

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/509,359DATE: 06/17/96
TIME: 10:08:37

INPUT SET: S11080.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E

ENTERED

(ii) TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE

(iii) NUMBER OF SEQUENCES: 160

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Testa, Hurwitz & Thibault
(B) STREET: High Street Tower - 125 High Street
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: U.S.A.
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/509,359
(B) FILING DATE: 31-JUL-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Twomey, Michael J
(B) REGISTRATION NUMBER: 38349

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 248-7362
(B) TELEFAX: (617) 248-7100

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2791 base pairs
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

55	TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA AAAAAACAGC GGCTGGTCTG	60
56		
57	GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGNAAGC GTATACCTAA	120
58		
59	TCTGGGAGCC TGCAAGTGAC AACAGCCTTT GCGGTCCTTA GACAGCTTGG CCTGGAGGAG	180
60		
61	AACACATGAA AGAAAGAACC TCAAGAGGCT TTGTTTTCTG TGAAACAGTA TTTCTATACA	240
62		
63	GTTGCTCCAA TGACAGAGTT ACCTGCACCG TTGTCCTACT TCCAGAATGC ACAGATGTCT	300
64		
65	GAGGACAACC ACCTGAGCAA TACTGTACGT AGCCAGAATG ACAATAGAGA ACGGCAGGAG	360
66		
67	CACAACGACA GACGGAGCCT TGGCCACCCT GAGCCATTAT CTAATGGACG ACCCCAGGGT	420
68		
69	AACTCCCGGC AGGTGGTGGA GCAAGATGAG GAAGAAGATG AGGAGCTGAC ATTGAAATAT	480
70		
71	GGCGCCAAGC ATGTGATCAT GCTCTTTGTC CCTGTGACTC TCTGCATGGT GGTGGTCGTG	540
72		
73	GCTACCATTA AGTCAGTCAG CTTTTATACC CGGAAGGATG GGCAGCTAAT CTATACCCCA	600
74		
75	TTCACAGAAG ATACCGAGAC TGTGGGCCAG AGAGCCCTGC ACTCAATTCT GAATGCTGCC	660
76		
77	ATCATGATCA GTGTCATTGT TGTCATGACT ATCCTCCTGG TGGTCTGTGA TAAATACAGG	720
78		
79	TGCTATAAGG TCATCCATGC CTGGCTTATT ATATCATCTC TATTGTTGCT GTTCTTTTTT	780
80		
81	TCATTCAATTT ACTTGGGGGA AGTGTTTAAA ACCTATAACG TTGCTGTGGA CTACATTACT	840
82		
83	GTTGCACTCC TGATCTGGAA TTTGGGTGTG GTGGGAATGA TTTCCATTCA CTGGAAAGGT	900
84		
85	CCACTTCGAC TCCAGCAGGC ATATCTCATT ATGATTAGTG CCCTCATGGC CCTGGTGTTT	960
86		
87	ATCAAGTACC TCCCTGAATG GACTGCGTGG CTCATCTTGG CTGTGATTTT AGTATATGAT	1020
88		
89	TTAGTGCGTG TTTTGTGTCC GAAAGGTCCA CTTGCTATGC TGGTTGAAAC AGCTCAGGAG	1080
90		
91	AGAAATGAAA CGCTTTTTTCC AGCTCTCATT TACTCCTCAA CAATGGTGTG GTTGGTGAAT	1140
92		
93	ATGGCAGAAG GAGACCCGGA AGCTCAAAGG AGAGTATCCA AAAATTCCAA GTATAATGCA	1200
94		
95	GAAAGCACAG AAAGGGAGTC ACAAGACACT GTTGACAGAGA ATGATGATGG CGGGTTCAGT	1260
96		
97	GAGGAATGGG AAGCCCAGAG GGACAGTCAT CTAGGGCCTC ATCGCTCTAC ACCTGAGTCA	1320
98		
99	CGAGCTGCTG TCCAGGAAC TTCCAGCAGT ATCCTCGCTG GTGAAGACCC AGAGGAAAGG	1380

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100								
101	GGAGTAAAC	TTGGATTGGG	AGATTTTCATT	TTCTACAGTG	TTCTGGTTGG	TAAAGCCTCA	1440	
102								
103	GCAACAGCCA	GTGGAGACTG	GAACACAACC	ATAGCCTGTT	TCGTAGCCAT	ATTAATTGGT	1500	
104								
105	TTGTGCCTTA	CATTATTACT	CCTTGCCATT	TTCAAGAAAG	CATTGCCAGC	TCTTCCAATC	1560	
106								
107	TCCATCACCT	TTGGGCTTGT	TTTCTACTTT	GCCACAGATT	ATCTTGTACA	GCCTTTTATG	1620	
108								
109	GACCAATTAG	CATTCCATCA	ATTTTATATC	TAGCATATTT	GCGGTTAGAA	TCCCATGGAT	1680	
110								
111	GTTTCTTCTT	TGACTATAAC	CAAACTCTGGG	GAGGACAAAG	GTGATTTTCC	TGTGTCCACA	1740	
112								
113	TCTAACAAAG	TCAAGATTCC	CGGCTGGACT	TTTGCAGCTT	CCTTCCAAGT	CTTCCTGACC	1800	
114								
115	ACCTTGCACT	ATTGGACTTT	GGAAGGAGGT	GCCTATAGAA	AACGATTTTG	AACATACTTC	1860	
116								
117	ATCGCAGTGG	ACTGTGTCCT	CGGTGCAGAA	ACTACCAGAT	TTGAGGGACG	AGGTCAAGGA	1920	
118								
119	GATATGATAG	GCCCCGAAGT	TGCTGTGCCC	CATCAGCAGC	TTGACGCGTG	GTCACAGGAC	1980	
120								
121	GATTTCACTG	ACACTGCGAA	CTCTCAGGAC	TACCGGTTAC	CAAGAGGTTA	GGTGAAGTGG	2040	
122								
123	TTTAAACCAA	ACGGAACCTC	TCATCTTAAA	CTACACGTTG	AAAATCAACC	CAATAATTCT	2100	
124								
125	GTATTAAGTG	AATTCTGAAC	TTTTCAGGAG	GTAAGTGAG	GAAGAGCAGG	CACCAGCAGC	2160	
126								
127	AGAATGGGGA	ATGGAGAGGT	GGGCAGGGGT	TCCAGCTTCC	CTTTGATTTT	TTGCTGCAGA	2220	
128								
129	CTCATCCTTT	TTAAATGAGA	CTTGTTTTCC	CCTCTCTTTG	AGTCAAGTCA	AATATGTAGA	2280	
130								
131	TGCCTTTGGC	AATTCTTCTT	CTCAAGCACT	GACACTCATT	ACCGTCTGTG	ATTGCCATTT	2340	
132								
133	CTTCCCAAGG	CCAGTCTGAA	CCTGAGGTTG	CTTTATCCTA	AAAGTTTTAA	CCTCAGGTTT	2400	
134								
135	CAAATTCAGT	AAATTTTGGG	AACAGTACAG	CTATTTCTCA	TCAATTCTCT	ATCATGTTGA	2460	
136								
137	AGTCAAATTT	GGATTTTCCA	CCAAATTCTG	AATTTGTAGA	CATACTTGTA	CGCTCACTTG	2520	
138								
139	CCCCAGATGC	CTCCTCTGTC	CTCATCTTTC	TCTCCACAC	AAGCAGTCTT	TTTCTACAGC	2580	
140								
141	CAGTAAGGCA	GCTCTGTCGT	GGTAGCAGAT	GGTCCCCTT	ATTCTAGGGT	CTTACTCTTT	2640	
142								
143	GTATGATGAA	AAGAATGTGT	TATGAATCGG	TGCTGTCAGC	CCTGCTGTCA	GACCTTCTTC	2700	
144								
145	CACAGCAAAT	GAGATGTATG	CCCAAAGCGG	TAGAATTAAA	GAAGAGTAAA	ATGGCTGTTG	2760	
146								
147	AAGCAAAAAA	AAAAAAAAAA	AAAAAAAAAA	A			2791	
148								
149								
150	(2)	INFORMATION	FOR	SEQ	ID	NO:2:		
151								
152	(i)	SEQUENCE	CHARACTERISTICS:					

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153      (A) LENGTH: 467 amino acids
154      (B) TYPE: amino acid
155      (C) STRANDEDNESS: single
156      (D) TOPOLOGY: linear
157
158
159      (ii) MOLECULE TYPE: protein
160
161      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
162
163      Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
164      1          5          10          15
165
166      Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
167      20          25          30
168
169      Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
170      35          40          45
171
172      Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
173      50          55          60
174
175      Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
176      65          70          75          80
177
178      His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
179      85          90          95
180
181      Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
182      100         105         110
183
184      Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
185      115         120         125
186
187      Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
188      130         135         140
189
190      Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
191      145         150         155         160
192
193      Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
194      165         170         175
195
196      Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
197      180         185         190
198
199      Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Leu Gly Val Val
200      195         200         205
201
202      Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
203      210         215         220
204
205      Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr

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206	225	230	235	240
207				
208	Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr			
209		245	250	255
210				
211	Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val			
212		260	265	270
213				
214	Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr			
215		275	280	285
216				
217	Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu			
218		290	295	300
219				
220	Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr			
221	305	310	315	320
222				
223	Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe			
224		325	330	335
225				
226	Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg			
227		340	345	350
228				
229	Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile			
230		355	360	365
231				
232	Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly			
233		370	375	380
234				
235	Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala			
236		385	390	395
237				400
238	Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile			
239		405	410	415
240				
241	Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu			
242		420	425	430
243				
244	Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala			
245		435	440	445
246				
247	Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln			
248		450	455	460
249				
250	Phe Tyr Ile			
251	465			
252				
253				
254				
255				
256	(2) INFORMATION FOR SEQ ID NO:3:			
257				
258	(i) SEQUENCE CHARACTERISTICS:			

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SEQUENCE VERIFICATION REPORT
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Original Text